

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Shyjan, Andrew W.
- (ii) TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
DIAGNOSIS, PREVENTION AND TREATMENT OF TUMOR  
PROGRESSION
- (iii) NUMBER OF SEQUENCES: 9
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Fish & Richardson P.C.  
(B) STREET: 225 Franklin Street  
(C) CITY: Boston  
(D) STATE: MA  
(E) COUNTRY: USA  
(F) ZIP: 02110-2804
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE: 23-MAY-1997  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/623,679  
(B) FILING DATE: 29-MAR-1996
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/412,431  
(B) FILING DATE: 29-MAR-1995
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Fasse, J. Peter  
(B) REGISTRATION NUMBER: 32,983  
(C) REFERENCE/DOCKET NUMBER: 07334/004002
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 617/542-5070  
(B) TELEFAX: 617/542-8906  
(C) TELEX: 200154

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 186 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGTGCTGGAG TACCTCATGG GCGGTGCCTA CCGCTGCAAC TACACTCGGA AAAGCTTCCG 60  
GACTCTCTAC AACAACTTGT TTGGCCCTAA GAGGGTAGAG CTCAGCAGAC ACACAGTGTC 120

036644 0539  
20050224

CTGTGCCTCC CAGAGTAACA TGTGGTTCCT TGATGTGCTT CCCCCAAAGC CCACCTGTGC 180  
AGAATG 186

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AAGGAGGCTA GGCTGCACCC TTCCCGCTTG CTCAGCAGCT GAGGCAGGGT CAGAAAGCAT 60  
GGATAGAGAA GACATTTTGC AAAAGGGAAT GCATCTTTGT AATTCCCAGT ACAAAGACC 120  
CTAACAGATG TTGCTGTGGT CAGCTACTA ACCAGCACAT CCCCCCTTTG CCGAGTGGGG 180  
CTCCCAGCAC AACAGGAGAG GACACCAAGC AGGCAGACAC GCAGTCCGGG AAATGGTCTG 240  
TCAGCAAACA CACCCAGAGC TACCCAACAG ACTCCTATGG GATTCTTGAA TTCCAGGGTG 300  
GGGGTTACTC CAATAAGCC ATG TAC ATC CGA GTC TCC TAC GAC ACC AAG 350  
Met Tyr Ile Arg Val Ser Tyr Asp Thr Lys  
1 5 10  
CCA GAT TCC CTG CTC CAC CTC ATG GTG AAG GAC TGG CAG CTG GAG CTC 398  
Pro Asp Ser Leu Leu His Leu Met Val Lys Asp Trp Gln Leu Glu Leu  
15 20 25  
CCG AAG CTC TTG ATA TCT GTG CAC GGA GGC CTC CAA AGC TTC GAG ATG 446  
Pro Lys Leu Leu Ile Ser Val His Gly Gly Leu Gln Ser Phe Glu Met  
30 35 40  
CAG TCC AAA CTG AAG CAG GTG TTT GGG AAA GGT CTG ATC AAG GCT GCC 494  
Gln Ser Lys Leu Lys Gln Val Phe Gly Lys Gly Leu Ile Lys Ala Ala  
45 50 55  
ATG ACC ACG GGG GCG TGG ATC TTC ACC GGG GGT GTG AGC ACT GGT GTC 542  
Met Thr Thr Gly Ala Trp Ile Phe Thr Gly Gly Val Ser Thr Gly Val  
60 65 70  
GTC AGC CAT GTG GGG GAT GCC TTG AAA GAC CAC TCC TCC AAG TCC AGA 590  
Val Ser His Val Gly Asp Ala Leu Lys Asp His Ser Ser Lys Ser Arg  
75 80 85 90  
GGC CGG CTC TGT GCT ATA GGA ATT GCT CCC TGG GGC ATG GTG GAG AAC 638  
Gly Arg Leu Cys Ala Ile Gly Ile Ala Pro Trp Gly Met Val Glu Asn  
95 100 105  
AAG GAA GAC CTG ATT GGA AAA GAT GTA ACA AGA GTC TAT CAG ACC ATG 686  
Lys Glu Asp Leu Ile Gly Lys Asp Val Thr Arg Val Tyr Gln Thr Met  
110 115 120  
TCC AAC CCT CTG AGC AAG CTC TCT GTG CTC AAC AAT TCC CAC ACT CAC 734  
Ser Asn Pro Leu Ser Lys Leu Ser Val Leu Asn Asn Ser His Thr His  
125 130 135  
TTC ATC TTG GCT GAC AAC GGC ACC CTG GGC AAG TAT GGT GCT GAG GTG 782  
Ph Ile Leu Ala Asp Asn Gly Thr Leu Gly Lys Tyr Gly Ala Glu Val  
140 145 150

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AAG CTT CGA AGA CAG CTG GAA AAA CAC ATC TCC CTG CAG AAG ATC AAC Lys Leu Arg Arg Gln L u Glu Lys His Ile Ser Leu Gln Lys Ile Asn 155 160 165 170	830
ACA AGG CTG GGC CAG GGT GTA CCT GTC GTG GGC CTA GTG GTA GAA GGT Thr Arg L u Gly Gln Gly Val Pro Val Val Gly Leu Val Val Glu Gly 175 180 185	878
GGT CCT AAC GTG GTT TCT ATC GTC CTG GAG TAT CTC AAA GAA GAC CCT Gly Pro Asn Val Val Ser Ile Val Leu Glu Tyr Leu Lys Glu Asp Pro 190 195 200	926
CCT GTC CCT GTG GTG GTT TGC GAT GGC AGT GGA CGT GCC TCT GAC ATT Pro Val Pro Val Val Val Cys Asp Gly Ser Gly Arg Ala Ser Asp Ile 205 210 215	974
TTG TCC TTC GCA CAC AAA TAC TGC GAC GAA GGA GGA GTC ATA AAC GAG Leu Ser Phe Ala His Lys Tyr Cys Asp Glu Gly Gly Val Ile Asn Glu 220 225 230	1022
TCC CTG CGG GAC CAG CTT CTA GTT ACC ATT CAG AAA ACA TTT AAT TAC Ser Leu Arg Asp Gln Leu Leu Val Thr Ile Gln Lys Thr Phe Asn Tyr 235 240 245 250	1070
AGC AAG TCC CAG TCG TAT CAG CTG TTT GCA ATT ATC ATG GAG TGC ATG Ser Lys Ser Gln Ser Tyr Gln Leu Phe Ala Ile Ile Met Glu Cys Met 255 260 265	1118
AAG AAG AAA GAA CTC GTC ACT GTG TTT CGG ATG GGT TCC GAG GGT CAG Lys Lys Lys Glu Leu Val Thr Val Phe Arg Met Gly Ser Glu Gly Gln 270 275 280	1166
CAA GAT GTC GAG ATG GCA ATT TTA ACT GCC TTG CTC AAA GGA ACC AAC Gln Asp Val Glu Met Ala Ile Leu Thr Ala Leu Leu Lys Gly Thr Asn 285 290 295	1214
GCA TCA GCT CCA GAT CAG CTG AGC TTG GCC CTG GCT TGG AAC CGG GTC Ala Ser Ala Pro Asp Gln Leu Ser Leu Ala Leu Ala Trp Asn Arg Val 300 305 310	1262
GAC ATA GCG CGA AGC CAG ATC TTC GTC TTT GGC CCA CAC TGG CCG CCA Asp Ile Ala Arg Ser Gln Ile Phe Val Phe Gly Pro His Trp Pro Pro 315 320 325 330	1310
CTG GGA AGC CTG GCC CCT CCT GTG GAC ACC AAA GCC GCA GAG AAG GAA Leu Gly Ser Leu Ala Pro Pro Val Asp Thr Lys Ala Ala Glu Lys Glu 335 340 345	1358
AAG AAG CCA CCC ACA GCC ACC ACC AAG GGG AGA GGA AAA GGA AAA GGC Lys Lys Pro Pro Thr Ala Thr Thr Lys Gly Arg Gly Lys Gly Lys Gly 350 355 360	1406
AAG AAG AAA GGC AAA GTG AAA GAG GAA GTG GAG GAA GAG ACG GAC CCC Lys Lys Lys Gly Lys Val Lys Glu Glu Val Glu Glu Glu Thr Asp Pro 365 370 375	1454
CGG AAG CTT GAG CTG CTC AAC TGG GTG AAT GCC CTG GAG CAA GCC ATG Arg Lys Leu Glu Leu Leu Asn Trp Val Asn Ala Leu Glu Gln Ala Met 380 385 390	1502
CTG GAT GCT CTT GTC CTA GAT CGG GTG GAC TTT GTA AAG CTC CTG ATT Leu Asp Ala Leu Val Leu Asp Arg Val Asp Phe Val Lys Leu Leu Ile 395 400 405 410	1550



(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Tyr	Ile	Arg	Val	Ser	Tyr	Asp	Thr	Lys	Pro	Asp	Ser	Leu	Leu	His
1				5					10					15	
Leu	Met	Val	Lys	Asp	Trp	Gln	Leu	Glu	Leu	Pro	Lys	Leu	Leu	Ile	Ser
		20					25						30		
Val	His	Gly	Gly	Leu	Gln	Ser	Phe	Glu	Met	Gln	Ser	Lys	Leu	Lys	Gln
		35					40					45			
Val	Phe	Gly	Lys	Gly	Leu	Ile	Lys	Ala	Ala	Met	Thr	Thr	Gly	Ala	Trp
	50					55					60				
Ile	Phe	Thr	Gly	Gly	Val	Ser	Thr	Gly	Val	Val	Ser	His	Val	Gly	Asp
	65				70					75					80
Ala	Leu	Lys	Asp	His	Ser	Ser	Lys	Ser	Arg	Gly	Arg	Leu	Cys	Ala	Ile
				85					90					95	
Gly	Ile	Ala	Pro	Trp	Gly	Met	Val	Glu	Asn	Lys	Glu	Asp	Leu	Ile	Gly
			100					105					110		
Lys	Asp	Val	Thr	Arg	Val	Tyr	Gln	Thr	Met	Ser	Asn	Pro	Leu	Ser	Lys
		115					120					125			
Leu	Ser	Val	Leu	Asn	Asn	Ser	His	Thr	His	Phe	Ile	Leu	Ala	Asp	Asn
	130					135					140				
Gly	Thr	Leu	Gly	Lys	Tyr	Gly	Ala	Glu	Val	Lys	Leu	Arg	Arg	Gln	Leu
	145				150					155					160
Glu	Lys	His	Ile	Ser	Leu	Gln	Lys	Ile	Asn	Thr	Arg	Leu	Gly	Gln	Gly
				165					170					175	
Val	Pro	Val	Val	Gly	Leu	Val	Val	Glu	Gly	Gly	Pro	Asn	Val	Val	Ser
			180					185					190		
Ile	Val	Leu	Glu	Tyr	Leu	Lys	Glu	Asp	Pro	Pro	Val	Pro	Val	Val	Val
		195					200					205			
Cys	Asp	Gly	Ser	Gly	Arg	Ala	Ser	Asp	Ile	Leu	Ser	Phe	Ala	His	Lys
	210					215					220				
Tyr	Cys	Asp	Glu	Gly	Gly	Val	Ile	Asn	Glu	Ser	Leu	Arg	Asp	Gln	Leu
	225				230					235					240
Leu	Val	Thr	Ile	Gln	Lys	Thr	Phe	Asn	Tyr	Ser	Lys	Ser	Gln	Ser	Tyr
				245					250					255	
Gln	Leu	Phe	Ala	Ile	Ile	Met	Glu	Cys	Met	Lys	Lys	Lys	Glu	Leu	Val
			260					265					270		
Thr	Val	Phe	Arg	Met	Gly	Ser	Glu	Gly	Gln	Gln	Asp	Val	Glu	Met	Ala
				275			280					285			

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Ile Leu Thr Ala L u Leu Lys Gly Thr Asn Ala Ser Ala Pro Asp Gln  
 290 295 300  
 Leu Ser Leu Ala Leu Ala Trp Asn Arg Val Asp Ile Ala Arg Ser Gln  
 305 310 315 320  
 Ile Phe Val Phe Gly Pro His Trp Pro Pro Leu Gly Ser Leu Ala Pro  
 325 330 335  
 Pro Val Asp Thr Lys Ala Ala Glu Lys Glu Lys Lys Pro Pro Thr Ala  
 340 345 350  
 Thr Thr Lys Gly Arg Gly Lys Gly Lys Gly Lys Lys Gly Lys Val  
 355 360 365  
 Lys Glu Glu Val Glu Glu Glu Thr Asp Pro Arg Lys Leu Glu Leu Leu  
 370 375 380  
 Asn Trp Val Asn Ala Leu Glu Gln Ala Met Leu Asp Ala Leu Val Leu  
 385 390 395 400  
 Asp Arg Val Asp Phe Val Lys Leu Leu Ile Glu Asn Gly Val Asn Met  
 405 410 415  
 Gln His Phe Leu Thr Ile Pro Arg Leu Glu Glu Leu Tyr Asn Thr Arg  
 420 425 430  
 Leu Gly Pro Pro Asn Thr Leu His Leu Leu Val Arg Asp Val Lys Lys  
 435 440 445  
 Ser Asn Leu Pro Pro Asp Tyr His Ile Ser Leu Ile Asp Ile Gly Leu  
 450 455 460  
 Val Leu Glu Tyr Leu Met Gly Gly Ala Tyr Arg Cys Asn Tyr Thr Arg  
 465 470 475 480  
 Lys Ser Phe Arg Thr Leu Tyr Asn Asn Leu Phe Gly Pro Lys Arg Val  
 485 490 495  
 Glu Leu Ser Arg His Thr Val Ser Cys Ala Ser Gln Ser Asn Met Trp  
 500 505 510  
 Phe Leu Asp Val Leu Pro Gln Lys Pro Thr Cys Ala Glu Cys Asn Ser  
 515 520 525  
 Ser Pro His Leu Ser Gln Thr Asp Ile Thr Pro Pro Leu Pro  
 530 535 540

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGGGAAGCAC ATCAAGGAAC

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 bas pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCAACTACTA CACTCGGAAA AGC

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(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4944 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 346..4837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ACTCATTATA GGGNTCGAGC GGCCGCCCCG GCAGGTTTGA GCTGTGCCCT CTCCATTCCA	60
CTGCTGTGGC AGGGTCAGAA ATCTTGATA GAGAAAACCT TTTGCAAACG GGAATGTATC	120
TTTGTAATTC CTAGCACGAA AGACTCTAAC AGGTGTTGCT GTGGCCAGTT CACCAACCAG	180
CATATCCCC CTCTGCCAAG TGCAACACCC AGCAAAAATG AAGAGGAAAG CAAACAGGTG	240
GAGACTCAGC CTGAGAAATG GTCTGTTGCC AAGCACACCC AGAGCTACCC AACAGATTCC	300
TATGGAGTTC TTGAATTCCA GGGTGGCGGA TATCCAATA AAGCC ATG TAT ATC	354
Met Tyr Ile	
1	
CGT GTA TCC TAT GAC ACC AAG CCA GAC TCA CTG CTC CAT CTC ATG GTG	402
Arg Val Ser Tyr Asp Thr Lys Pro Asp Ser Leu Leu His Leu Met Val	
5 10 15	
AAA GAT TGG CAG CTG GAA CTC CCC AAG CTC TTA ATA TCT GTG CAT GGA	450
Lys Asp Trp Gln Leu Glu Leu Pro Lys Leu Leu Ile Ser Val His Gly	
20 25 30 35	
GGC CTC CAG AAC TTT GAG ATG CAG CCC AAG CTG AAA CAA GTC TTT GGG	498
Gly Leu Gln Asn Phe Glu Met Gln Pro Lys Leu Lys Gln Val Phe Gly	
40 45 50	
AAA GGC CTG ATC AAG GCT GCT ATG ACC ACC GGG GCC TGG ATC TTC ACC	546
Lys Gly Leu Ile Lys Ala Ala Met Thr Thr Gly Ala Trp Ile Phe Thr	
55 60 65	
GGG GGT GTC AGC ACA GGT GTT ATC AGC CAC GTA GGG GAT GCC TTG AAA	594
Gly Gly Val Ser Thr Gly Val Ile Ser His Val Gly Asp Ala Leu Lys	
70 75 80	
GAC CAC TCC TCC AAG TCC AGA GGC CGG GTT TGT GCT ATA GGA ATT GCT	642
Asp His S r S r Lys Ser Arg Gly Arg Val Cys Ala Il Gly Ile Ala	
85 90 95	

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2442980

CCA Pro 100	TGG Trp	GGC Gly	ATC Ile	GTG Val	GAG Glu 105	AAT Asn	AAG Lys	GAA Glu	GAC Asp	CTG Leu 110	GTT Val	GGA Gly	AAG Lys	GAT Asp	GTA Val 115	690
ACA Thr	AGA Arg	GTG Val	TAC Tyr	CAG Gln 120	ACC Thr	ATG Met	TCC Ser	AAC Asn	CCT Pro 125	CTA Leu	AGT Ser	AAG Lys	CTC L u	TCT Ser 130	GTG Val	738
CTC Leu	AAC Asn	AAC Asn	TCC Ser 135	CAC His	ACC Thr	CAC His	TTC Phe	ATC Ile 140	CTG Leu	GCT Ala	GAC Asp	AAT Asn	GGC Gly 145	ACC Thr	CTG Leu	786
GGC Gly	AAG Lys	TAT Tyr 150	GGC Gly	GCC Ala	GAG Glu	GTG Val	AAG Lys 155	CTG Leu	CGA Arg	AGG Arg	CTG Leu 160	CTG Leu	GAA Glu	AAG Lys	CAC His	834
ATC Ile	TCC Ser 165	CTC Leu	CAG Gln	AAG Lys	ATC Ile	AAC Asn 170	ACA Thr	AGA Arg	CTG Leu	GGG Gly 175	CAG Gln	GGC Gly	GTG Val	CCC Pro	CTC Leu	882
GTG Val 180	GGT Gly	CTC Leu	GTG Val	GTG Val	GAG Glu 185	GGG Gly	GGC Gly	CCT Pro	AAC Asn	GTG Val 190	GTG Val	TCC Ser	ATC Ile	GTC Val	TTG Leu 195	930
GAA Glu	TAC Tyr	CTG Leu	CAA Gln 200	GAA Glu	GAG Glu	CCT Pro	CCC Pro	ATC Ile	CCT Pro 205	GTG Val	GTG Val	ATT Ile	TGT Cys	GAT Asp 210	GGC Gly	978
AGC Ser	GGA Gly	CGT Arg	GCC Ala 215	TCG Ser	GAC Asp	ATC Ile	CTG Leu	TCC Ser 220	TTT Phe	GCG Ala	CAC His	AAG Lys	TAC Tyr 225	TGT Cys	GAA Glu	1026
GAA Glu	GGC Gly	GGA Gly 230	ATA Ile	ATA Ile	AAT Asn	GAG Glu	TCC Ser 235	CTC Leu	AGG Arg	GAG Glu	CAG Gln	CTT Leu 240	CTA Leu	GTT Val	ACC Thr	1074
ATT Ile	CAG Gln 245	AAA Lys	ACA Thr	TTT Phe	AAT Asn	TAT Tyr 250	AAT Asn	AAG Lys	GCA Ala	CAA Gln	TCA Ser 255	CAT His	CAG Gln	CTG Leu	TTT Phe	1122
GCA Ala 260	ATT Ile	ATA Ile	ATG Met	GAG Glu	TGC Cys 265	ATG Met	AAG Lys	AAG Lys	AAA Lys	GAA Glu 270	CTC Leu	GTC Val	ACT Thr	GTG Val	TTT Phe 275	1170
AGA Arg	ATG Met	GGT Gly	TCT Ser 280	GAG Glu	GGC Gly	CAG Gln	CAG Gln	GAC Asp	ATC Ile 285	GAG Glu	ATG Met	GCA Ala	ATT Ile	TTA Leu 290	ACT Thr	1218
GCC Ala	CTG Leu	CTG Leu	AAA Lys 295	GGA Gly	ACA Thr	AAC Asn	GTA Val	TCT Ser 300	GCT Ala	CCA Pro	GAT Asp	CAG Gln	CTG Leu 305	AGC Ser	TTG Leu	1266
GCA Ala	CTG Leu	GCT Ala 310	TGG Trp	AAC Asn	CGC Arg	GTG Val	GAC Asp 315	ATA Ile	GCA Ala	CGA Arg	AGC Ser	CAG Gln 320	ATC Ile	TTT Phe	GTC Val	1314
TTT Phe	GGG Gly 325	CCC Pro	CAC His	TGG Trp	ACG Thr	CCC Pro 330	CTG Leu	GGA Gly	AGC Ser	CTG Leu	GCA Ala 335	CCC Pro	CCG Pro	ACG Thr	GAC Asp	1362
AGC Ser 340	AAA Lys	GCC Ala	ACG Thr	GAG Glu	AAG Lys 345	GAG Glu	AAG Lys	AAG Lys	CCA Pro	CCC Pro 350	ATG Met	GCC Ala	ACC Thr	ACC Thr	AAG Lys 355	1410



GGA Gly	GGA Gly	AGA Arg	GGA Gly	AAA Lys 360	GGG Gly	AAA Lys	GGC Gly	AAG Lys	AAG Lys 365	AAA Lys	GGG Gly	AAA Lys	GTG Val	AAA Lys 370	GAG Glu	1458
GAA Glu	GTG Val	GAG Glu	GAA Glu 375	GAA Glu	ACT Thr	GAC Asp	CCC Pro	CGG Arg 380	AAG Lys	ATA Ile	GAG Glu	CTG Leu	CTG Leu 385	AAC Asn	TGG Trp	1506
GTG Val	AAT Asn	GCT Ala 390	TTG Leu	GAG Glu	CAA Gln	GCG Ala	ATG Met 395	CTA Leu	GAT Asp	GCT Ala	TTA Leu	GTC Val 400	TTA Leu	GAT Asp	CGT Arg	1554
GTC Val	GAC Asp 405	TTT Phe	GTG Val	AAG Lys	CTC Leu	CTG Leu 410	ATT Ile	GAA Glu	AAC Asn	GGA Gly	GTG Val 415	AAC Asn	ATG Met	CAA Gln	CAC His	1602
TTT Phe 420	CTG Leu	ACC Thr	ATT Ile	CCG Pro	AGG Arg 425	CTG Leu	GAG Glu	GAG Glu	CTT Leu	TAT Tyr 430	AAC Asn	ACA Thr	AGA Arg	CTG Leu	GGT Gly 435	1650
CCA Pro	CCA Pro	AAC Asn	ACA Thr	CTT Leu 440	CAT His	CTG Leu	CTG Leu	GTG Val	AGG Arg 445	GAT Asp	GTG Val	AAA Lys	AAG Lys	AGC Ser 450	AAC Asn	1698
CTT Leu	CCG Pro	CCT Pro	GAT Asp 455	TAC Tyr	CAC His	ATC Ile	AGC Ser	CTC Leu 460	ATA Ile	GAC Asp	ATC Ile	GGG Gly	CTC Leu 465	GTG Val	CTG Leu	1746
GAG Glu	TAC Tyr	CTC Leu 470	ATG Met	GGA Gly	GGA Gly	GCC Ala	TAC Tyr 475	CGC Arg	TGC Cys	AAC Asn	TAC Tyr	ACT Thr 480	CGG Arg	AAA Lys	AAC Asn	1794
TTT Phe	CGG Arg 485	ACC Thr	CTT Leu	TAC Tyr	AAC Asn	AAC Asn 490	TTG Leu	TTT Phe	GGA Gly	CCA Pro	AAG Lys 495	AGG Arg	CCT Pro	AAA Lys	GCT Ala	1842
CTT Leu 500	AAA Lys	CTT Leu	CTG Leu	GGA Gly	ATG Met 505	GAA Glu	GAT Asp	GAT Asp	GAG Glu	CCT Pro 510	CCA Pro	GCT Ala	AAA Lys	GGG Gly	AAG Lys 515	1890
AAA Lys	AAA Lys	AAA Lys	AAA Lys	AAG Lys 520	AAA Lys	AAG Lys	GAG Glu	GAA Glu	GAG Glu 525	ATC Ile	GAC Asp	ATT Ile	GAT Asp	GTG Val 530	GAC Asp	1938
GAC Asp	CCT Pro	GCC Ala	GTG Val 535	AGT Ser	CGG Arg	TTC Phe	CAG Gln	TAT Tyr 540	CCC Pro	TTC Phe	CAC His	GAG Glu	CTG Leu 545	ATG Met	GTG Val	1986
TGG Trp	GCA Ala	GTG Val 550	CTG Leu	ATG Met	AAA Lys	CGC Arg	CAG Gln 555	AAA Lys	ATG Met	GCA Ala	GTG Val	TTC Phe 560	CTC Leu	TGG Trp	CAG Gln	2034
CGA Arg	GGG Gly 565	GAA Glu	GAG Glu	AGC Ser	ATG Met	GCC Ala 570	AAG Lys	GCC Ala	CTG Leu	GTG Val	GCC Ala 575	TGC Cys	AAG Lys	CTC Leu	TAC Tyr	2082
AAG Lys 580	GCC Ala	ATG Met	GCC Ala	CAC His	GAG Glu 585	TCC Ser	TCC Ser	GAG Glu	AGT Ser	GAT Asp 590	CTG Leu	GTG Val	GAT Asp	GAC Asp	ATC Ile 595	2130
TCC Ser	CAG Gln	GAC Asp	TTG Leu	GAT Asp 600	AAC Asn	AAT Asn	TCC Ser	AAA Lys	GAC Asp 605	TTC Phe	GGC Gly	CAG Gln	CTT Leu	GCT Ala 610	TTG Leu	2178



CTG GTC GTG CTC ATG AGT TTC GGA GTA GCC CGT CAA GCC ATT CTG CAT Leu Val Val Leu Met Ser Ph Gly Val Ala Arg Gln Ala Ile Leu His 870 880	2994
CCA GAG GAG AAG CCC TCT TGG AAA CTG GCC CGA AAC ATC TTC TAC ATG Pro Glu Glu Lys Pro Ser Trp Lys Leu Ala Arg Asn Ile Phe Tyr Met 885 890 895	3042
CCC TAC TGG ATG ATC TAT GGA GAG GTG TTT GCA GAC CAG ATA GAC CTC Pro Tyr Trp Met Ile Tyr Gly Glu Val Phe Ala Asp Gln Ile Asp Leu 900 905 910 915	3090
TAC GCC ATG GAA ATT AAT CCT CCT TGT GGT GAG AAC CTA TAT GAT GAG Tyr Ala Met Glu Ile Asn Pro Pro Cys Gly Glu Asn Leu Tyr Asp Glu 920 925 930	3138
GAG GGC AAG CGG CTT CCT CCC TGT ATC CCC GGC GCC TGG CTC ACT CCA Glu Gly Lys Arg Leu Pro Pro Cys Ile Pro Gly Ala Trp Leu Thr Pro 935 940 945	3186
GCA CTC ATG GCG TGC TAT CTA CTG GTC GCC AAC ATC CTG CTG GTG AAC Ala Leu Met Ala Cys Tyr Leu Leu Val Ala Asn Ile Leu Leu Val Asn 950 955 960	3234
CTG CTG ATT GCT GTG TTC AAC AAT ACC TTC TTT GAA GTA AAA TCA ATA Leu Leu Ile Ala Val Phe Asn Asn Thr Phe Phe Glu Val Lys Ser Ile 965 970 975	3282
TCC AAC CAG GTG TGG AAG TTC CAG CGA TAT CAG CTG ATT ATG ACA TTT Ser Asn Gln Val Trp Lys Phe Gln Arg Tyr Gln Leu Ile Met Thr Phe 980 985 990 995	3330
CAT GAC AGG CCA GTC CTG CCC CCA CCG ATG ATC ATT TTA AGC CAC ATC His Asp Arg Pro Val Leu Pro Pro Pro Met Ile Ile Leu Ser His Ile 1000 1005 1010	3378
TAC ATC ATC ATT ATG CGT CTC AGC GGC CGC TGC AGG AAA AAG AGA GAA Tyr Ile Ile Ile Met Arg Leu Ser Gly Arg Cys Arg Lys Lys Arg Glu 1015 1020 1025	3426
GGG GAC CAA GAG GAA CGG GAT CGT GGA TTG AAG CTC TTC CTT AGC GAC Gly Asp Gln Glu Glu Arg Asp Arg Gly Leu Lys Leu Phe Leu Ser Asp 1030 1035 1040	3474
GAG GAG CTA AAG AGG CTG CAT GAG TTC GAG GAG CAG TGC GTG CAG GAG Glu Glu Leu Lys Arg Leu His Glu Phe Glu Glu Gln Cys Val Gln Glu 1045 1050 1055	3522
CAC TTC CGG GAG AAG GAG GAT GAG CAG CAG TCG TCC AGC GAC GAG CGC His Phe Arg Glu Lys Glu Asp Glu Gln Gln Ser Ser Ser Asp Glu Arg 1060 1065 1070 1075	3570
ATC CGG GTC ACT TCT GAA AGA GTT GAA AAT ATG TCA ATG AGG TTG GAA Ile Arg Val Thr Ser Glu Arg Val Glu Asn Met Ser Met Arg Leu Glu 1080 1085 1090	3618
GAA ATC AAT GAA AGA GAA ACT TTT ATG AAA ACT TCC CTG CAG ACT GTT Glu Ile Asn Glu Arg Glu Thr Phe Met Lys Thr Ser Leu Gln Thr Val 1095 1100 1105	3666
GAC CTT CGA CTT GCT CAG CTA GAA GAA TTA TCT AAC AGA ATG GTG AAT Asp L u Arg Leu Ala Gln L u Glu Glu Leu S r Asn Arg M t Val Asn 1110 1115 1120	3714

GCT CTT GAA AAT CTT GCG GGA ATC GAC AGG TCT GAC CTG ATC CAG GCA Ala Leu Glu Asn Leu Ala Gly Ile Asp Arg Ser Asp Leu Ile Gln Ala 1125 1130 1135	3762
CGG TCC CGG GCT TCT TCT GAA TGT GAG GCA ACG TAT CTT CTC CGG CAA Arg Ser Arg Ala S r Ser Glu Cys Glu Ala Thr Tyr Leu L u Arg Gln 1140 1145 1150 1155	3810
AGC AGC ATC AAT AGC GCT GAT GGC TAC AGC TTG TAT CGA TAT CAT TTT Ser Ser Ile Asn Ser Ala Asp Gly Tyr Ser Leu Tyr Arg Tyr His Phe 1160 1165 1170	3858
AAC GGA GAA GAG TTA TTA TTT GAG GAT ACA TCT CTC TCC ACG TCA CCA Asn Gly Glu Glu Leu Leu Phe Glu Asp Thr Ser Leu Ser Thr Ser Pro 1175 1180 1185	3906
GGG ACA GGA GTC AGG AAA AAA ACC TGT TCC TTC CGT ATA AAG GAA GAG Gly Thr Gly Val Arg Lys Lys Thr Cys Ser Phe Arg Ile Lys Glu Glu 1190 1195 1200	3954
AAG GAC GTG AAA ACG CAC CTA GTC CCA GAA TGT CAG AAC AGT CTT CAC Lys Asp Val Lys Thr His Leu Val Pro Glu Cys Gln Asn Ser Leu His 1205 1210 1215	4002
CTT TCA CTG GGC ACA AGC ACA TCA GCA ACC CCA GAT GGC AGT CAC CTT Leu Ser Leu Gly Thr Ser Thr Ser Ala Thr Pro Asp Gly Ser His Leu 1220 1225 1230 1235	4050
GCA GTA GAT GAC TTA AAG AAC GCT GAA GAG TCA AAA TTA GGT CCA GAT Ala Val Asp Asp Leu Lys Asn Ala Glu Ser Lys Leu Gly Pro Asp 1240 1245 1250	4098
ATT GGG ATT TCA AAG GAA GAT GAT GAA AGA CAG ACA GAC TCT AAA AAA Ile Gly Ile Ser Lys Glu Asp Asp Glu Arg Gln Thr Asp Ser Lys Lys 1255 1260 1265	4146
GAA GAA ACT ATT TCC CCA AGT TTA AAT AAA ACA GAT GTG ATA CAT GGA Glu Glu Thr Ile Ser Pro Ser Leu Asn Lys Thr Asp Val Ile His Gly 1270 1275 1280	4194
CAG GAC AAA TCA GAT GTT CAA AAC ACT CAG CTA ACA GTG GAA ACG ACA Gln Asp Lys Ser Asp Val Gln Asn Thr Gln Leu Thr Val Glu Thr Thr 1285 1290 1295	4242
AAT ATA GAA GGC ACT ATT TCC TAT CCC CTG GAA GAA ACC AAA ATT ACA Asn Ile Glu Gly Thr Ile Ser Tyr Pro Leu Glu Glu Thr Lys Ile Thr 1300 1305 1310 1315	4290
CGC TAT TTC CCC GAT GAA ACG ATC AAT GCT TGT AAA ACA ATG AAG TCC Arg Tyr Phe Pro Asp Glu Thr Ile Asn Ala Cys Lys Thr Met Lys Ser 1320 1325 1330	4338
AGA AGC TTC GTC TAT TCC CGG GGA AGA AAG CTG GTC GGT GGG GTT AAC Arg Ser Phe Val Tyr Ser Arg Gly Arg Lys Leu Val Gly Gly Val Asn 1335 1340 1345	4386
CAG GAT GTA GAG TAC AGT TCA ATC ACG GAC CAG CAA TTG ACG ACG GAA Gln Asp Val Glu Tyr Ser Ser Ile Thr Asp Gln Gln Leu Thr Thr Glu 1350 1355 1360	4434
TGG CAA TGC CAA GTT CAA AAG ATC ACG CGC TCT CAT AGC ACA GAT ATT Trp Gln Cys Gln Val Gln Lys Ile Thr Arg Ser His S r Thr Asp Il 1365 1370 1375	4482

CCT TAC ATT GTG TCG GAA GCT GCA GTG CAA GCT GAG CAA AAA GAG CAG Pro Tyr Ile Val S r Glu Ala Ala Val Gln Ala Glu Gln Lys Glu Gln 1380 1385 1390 1395	4530
TTT GCA GAT ATG CAA GAT GAA CAC CAT GTC GCT GAA GCA ATT CCT CGA Phe Ala Asp Met Gln Asp Glu His His Val Ala Glu Ala Ile Pro Arg 1400 1405 1410	4578
ATC CCT CGC TTG TCC CTA ACC ATT ACT GAC AGA AAT GGG ATG GAA AAC Ile Pro Arg Leu Ser Leu Thr Ile Thr Asp Arg Asn Gly Met Glu Asn 1415 1420 1425	4626
TTA CTG TCT GTG AAG CCA GAT CAA ACT TTG GGA TTC CCA TCT CTC AGG Leu Leu Ser Val Lys Pro Asp Gln Thr Leu Gly Phe Pro Ser Leu Arg 1430 1435 1440	4674
TCA AAA AGT TTA CAT GGA CAT CCT AGG AAT GTG AAA TCC ATT CAG GGA Ser Lys Ser Leu His Gly His Pro Arg Asn Val Lys Ser Ile Gln Gly 1445 1450 1455	4722
AAG TTA GAC AGA TCT GGA CAT GCC AGT AGT GTA AGC AGC TTA GTA ATT Lys Leu Asp Arg Ser Gly His Ala Ser Ser Val Ser Ser Leu Val Ile 1460 1465 1470 1475	4770
GTG TCT GGA ATG ACA GCA GAA GAA AAA AAG GTT AAG AAA GAG AAA GCT Val Ser Gly Met Thr Ala Glu Glu Lys Lys Val Lys Lys Glu Lys Ala 1480 1485 1490	4818
TCC ACA GAA ACT GAA TGC T AGTCTGTTTT GTTCTTTAA TTTTTTTTTT Ser Thr Glu Thr Glu Cys 1495	4867
TAACAGTCAG AACCACTAAT GGGTGTGATC TTGGCCATCC TAAACATCCA TCCAATTTC	4927
TAAAAACATT TTCCCTT	4944

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1497 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Tyr Ile Arg Val Ser Tyr Asp Thr Lys Pro Asp Ser Leu Leu His 1 5 10 15
Leu Met Val Lys Asp Trp Gln Leu Glu Leu Pro Lys Leu Leu Ile Ser 20 25 30
Val His Gly Gly Leu Gln Asn Phe Glu Met Gln Pro Lys Leu Lys Gln 35 40 45
Val Phe Gly Lys Gly Leu Ile Lys Ala Ala Met Thr Thr Gly Ala Trp 50 55 60
Ile Phe Thr Gly Gly Val Ser Thr Gly Val Ile Ser His Val Gly Asp 65 70 75 80
Ala L u Lys Asp His Ser Ser Lys S r Arg Gly Arg Val Cys Ala Il 85 90 95

Gly Ile Ala Pro Trp Gly Ile Val Glu Asn Lys Glu Asp L u Val Gly  
 100 105 110  
 Lys Asp Val Thr Arg Val Tyr Gln Thr Met Ser Asn Pro Leu S r Lys  
 115 120 125  
 Leu Ser Val Leu Asn Asn Ser His Thr His Phe Ile Leu Ala Asp Asn  
 130 135 140  
 Gly Thr Leu Gly Lys Tyr Gly Ala Glu Val Lys Leu Arg Arg Leu Leu  
 145 150 155 160  
 Glu Lys His Ile Ser Leu Gln Lys Ile Asn Thr Arg Leu Gly Gln Gly  
 165 170 175  
 Val Pro Leu Val Gly Leu Val Val Glu Gly Gly Pro Asn Val Val Ser  
 180 185 190  
 Ile Val Leu Glu Tyr Leu Gln Glu Glu Pro Pro Ile Pro Val Val Ile  
 195 200 205  
 Cys Asp Gly Ser Gly Arg Ala Ser Asp Ile Leu Ser Phe Ala His Lys  
 210 215 220  
 Tyr Cys Glu Glu Gly Gly Ile Ile Asn Glu Ser Leu Arg Glu Gln Leu  
 225 230 235 240  
 Leu Val Thr Ile Gln Lys Thr Phe Asn Tyr Asn Lys Ala Gln Ser His  
 245 250 255  
 Gln Leu Phe Ala Ile Ile Met Glu Cys Met Lys Lys Lys Glu Leu Val  
 260 265 270  
 Thr Val Phe Arg Met Gly Ser Glu Gly Gln Gln Asp Ile Glu Met Ala  
 275 280 285  
 Ile Leu Thr Ala Leu Leu Lys Gly Thr Asn Val Ser Ala Pro Asp Gln  
 290 295 300  
 Leu Ser Leu Ala Leu Ala Trp Asn Arg Val Asp Ile Ala Arg Ser Gln  
 305 310 315 320  
 Ile Phe Val Phe Gly Pro His Trp Thr Pro Leu Gly Ser Leu Ala Pro  
 325 330 335  
 Pro Thr Asp Ser Lys Ala Thr Glu Lys Glu Lys Lys Pro Pro Met Ala  
 340 345 350  
 Thr Thr Lys Gly Gly Arg Gly Lys Gly Lys Gly Lys Lys Gly Lys  
 355 360 365  
 Val Lys Glu Glu Val Glu Glu Glu Thr Asp Pro Arg Lys Ile Glu Leu  
 370 375 380  
 Leu Asn Trp Val Asn Ala Leu Glu Gln Ala Met Leu Asp Ala Leu Val  
 385 390 395 400  
 Leu Asp Arg Val Asp Phe Val Lys Leu Leu Ile Glu Asn Gly Val Asn  
 405 410 415  
 M t Gln His Ph Leu Thr Ile Pro Arg Leu Glu Glu Leu Tyr Asn Thr  
 420 425 430

26339 "2429880  
 088644 05339

Arg Leu Gly Pro Pro Asn Thr Leu His Leu Leu Val Arg Asp Val Lys  
435 440 445

Lys Ser Asn Leu Pro Pro Asp Tyr His Ile S r Leu Ile Asp Ile Gly  
450 455 460

Leu Val Leu Glu Tyr Leu Met Gly Gly Ala Tyr Arg Cys Asn Tyr Thr  
465 470 475 480

Arg Lys Asn Phe Arg Thr Leu Tyr Asn Asn Leu Phe Gly Pro Lys Arg  
485 490 495

Pro Lys Ala Leu Lys Leu Leu Gly Met Glu Asp Asp Glu Pro Pro Ala  
500 505 510

Lys Gly Lys Lys Lys Lys Lys Lys Lys Lys Glu Glu Glu Ile Asp Ile  
515 520 525

Asp Val Asp Asp Pro Ala Val Ser Arg Phe Gln Tyr Pro Phe His Glu  
530 535 540

Leu Met Val Trp Ala Val Leu Met Lys Arg Gln Lys Met Ala Val Phe  
545 550 555 560

Leu Trp Gln Arg Gly Glu Glu Ser Met Ala Lys Ala Leu Val Ala Cys  
565 570 575

Lys Leu Tyr Lys Ala Met Ala His Glu Ser Ser Glu Ser Asp Leu Val  
580 585 590

Asp Asp Ile Ser Gln Asp Leu Asp Asn Asn Ser Lys Asp Phe Gly Gln  
595 600 605

Leu Ala Leu Glu Leu Leu Asp Gln Ser Tyr Lys His Asp Glu Gln Ile  
610 615 620

Ala Met Lys Leu Leu Thr Tyr Glu Leu Lys Asn Trp Ser Asn Ser Thr  
625 630 635 640

Cys Leu Lys Leu Ala Val Ala Ala Lys His Arg Asp Phe Ile Ala His  
645 650 655

Thr Cys Ser Gln Met Leu Leu Thr Asp Met Trp Met Gly Arg Leu Arg  
660 665 670

Met Arg Lys Asn Pro Gly Leu Lys Val Ile Met Gly Ile Leu Leu Pro  
675 680 685

Pro Thr Ile Leu Phe Leu Glu Phe Arg Thr Tyr Asp Asp Phe Ser Tyr  
690 695 700

Gln Thr Ser Lys Glu Asn Glu Asp Gly Lys Glu Lys Glu Glu Glu Asn  
705 710 715 720

Thr Asp Ala Asn Ala Asp Ala Gly Ser Arg Lys Gly Asp Glu Glu Asn  
725 730 735

Glu His Lys Lys Gln Arg Ile Ile Pro Ile Gly Thr Lys Ile Cys Lys  
740 745 750

Phe Tyr Asn Ala Pro Ile Val Lys Phe Trp Phe Tyr Thr Il S r Tyr  
755 760 765







Ser Leu Arg S r Lys Ser Leu His Gly His Pro Arg Asn Val Lys Ser  
1445 1450 1455

Il Gln Gly Lys Leu Asp Arg Ser Gly His Ala Ser Ser Val Ser Ser  
1460 1465 1470

Leu Val Ile Val Ser Gly Met Thr Ala Glu Glu Lys Lys Val Lys Lys  
1475 1480 1485

Glu Lys Ala Ser Thr Glu Thr Glu Cys  
1490 1495

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5055 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 346..4945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ACTCATTATA GGGNTCGAGC GGCCGCCCGG GCAGGTTTGA GCTGTGCCCT CTCCATTCCA	60
CTGCTGTGGC AGGGTCAGAA ATCTTGGATA GAGAAAACCT TTTGCAAACG GGAATGTATC	120
TTTGTAATTC CTAGCACGAA AGACTCTAAC AGGTGTTGCT GTGGCCAGTT CACCAACCAG	180
CATATCCCCC CTCTGCCAAG TGCAACACCC AGCAAAAATG AAGAGGAAAG CAAACAGGTG	240
GAGACTCAGC CTGAGAAATG GTCTGTTGCC AAGCACACCC AGAGCTACCC AACAGATTCC	300
TATGGAGTTC TTGAATTCCA GGGTGGCGGA TATTCCAATA AAGCC ATG TAT ATC	354
Met Tyr Ile	
1	
CGT GTA TCC TAT GAC ACC AAG CCA GAC TCA CTG CTC CAT CTC ATG GTG	402
Arg Val Ser Tyr Asp Thr Lys Pro Asp Ser Leu Leu His Leu Met Val	
5 10 15	
AAA GAT TGG CAG CTG GAA CTC CCC AAG CTC TTA ATA TCT GTG CAT GGA	450
Lys Asp Trp Gln Leu Glu Leu Pro Lys Leu Leu Ile Ser Val His Gly	
20 25 30 35	
GGC CTC CAG AAC TTT GAG ATG CAG CCC AAG CTG AAA CAA GTC TTT GGG	498
Gly Leu Gln Asn Phe Glu Met Gln Pro Lys Leu Lys Gln Val Phe Gly	
40 45 50	
AAA GGC CTG ATC AAG GCT GCT ATG ACC ACC GGG GCC TGG ATC TTC ACC	546
Lys Gly Leu Ile Lys Ala Ala Met Thr Thr Gly Ala Trp Ile Phe Thr	
55 60 65	
GGG GGT GTC AGC ACA GGT GTT ATC AGC CAC GTA GGG GAT GCC TTG AAA	594
Gly Gly Val S r Thr Gly Val Il S r His Val Gly Asp Ala L u Lys	
70 75 80	

2429330

GAC CAC TCC TCC AAG TCC AGA GGC CGG GTT TGT GCT ATA GGA ATT GCT Asp His S r Ser Lys S r Arg Gly Arg Val Cys Ala Ile Gly Ile Ala 85 90 95	642
CCA TGG GGC ATC GTG GAG AAT AAG GAA GAC CTG GTT GGA AAG GAT GTA Pro Trp Gly Ile Val Glu Asn Lys Glu Asp Leu Val Gly Lys Asp Val 100 105 110 115	690
ACA AGA GTG TAC CAG ACC ATG TCC AAC CCT CTA AGT AAG CTC TCT GTG Thr Arg Val Tyr Gln Thr Met Ser Asn Pro Leu Ser Lys Leu Ser Val 120 125 130	738
CTC AAC AAC TCC CAC ACC CAC TTC ATC CTG GCT GAC AAT GGC ACC CTG Leu Asn Asn Ser His Thr His Phe Ile Leu Ala Asp Asn Gly Thr Leu 135 140 145	786
GGC AAG TAT GGC GCC GAG GTG AAG CTG CGA AGG CTG CTG GAA AAG CAC Gly Lys Tyr Gly Ala Glu Val Lys Leu Arg Arg Leu Leu Glu Lys His 150 155 160	834
ATC TCC CTC CAG AAG ATC AAC ACA AGA CTG GGG CAG GGC GTG CCC CTC Ile Ser Leu Gln Lys Ile Asn Thr Arg Leu Gly Gln Gly Val Pro Leu 165 170 175	882
GTG GGT CTC GTG GTG GAG GGG GGC CCT AAC GTG GTG TCC ATC GTC TTG Val Gly Leu Val Val Glu Gly Gly Pro Asn Val Val Ser Ile Val Leu 180 185 190 195	930
GAA TAC CTG CAA GAA GAG CCT CCC ATC CCT GTG GTG ATT TGT GAT GGC Glu Tyr Leu Gln Glu Glu Pro Pro Ile Pro Val Val Ile Cys Asp Gly 200 205 210	978
AGC GGA CGT GCC TCG GAC ATC CTG TCC TTT GCG CAC AAG TAC TGT GAA Ser Gly Arg Ala Ser Asp Ile Leu Ser Phe Ala His Lys Tyr Cys Glu 215 220 225	1026
GAA GGC GGA ATA ATA AAT GAG TCC CTC AGG GAG CAG CTT CTA GTT ACC Glu Gly Gly Ile Ile Asn Glu Ser Leu Arg Glu Gln Leu Leu Val Thr 230 235 240	1074
ATT CAG AAA ACA TTT AAT TAT AAT AAG GCA CAA TCA CAT CAG CTG TTT Ile Gln Lys Thr Phe Asn Tyr Asn Lys Ala Gln Ser His Gln Leu Phe 245 250 255	1122
GCA ATT ATA ATG GAG TGC ATG AAG AAG AAA GAA CTC GTC ACT GTG TTC Ala Ile Ile Met Glu Cys Met Lys Lys Lys Glu Leu Val Thr Val Phe 260 265 270 275	1170
AGA ATG GGT TCT GAG GGC CAG CAG GAC ATC GAG ATG GCA ATT TTA ACT Arg Met Gly Ser Glu Gly Gln Gln Asp Ile Glu Met Ala Ile Leu Thr 280 285 290	1218
GCC CTG CTG AAA GGA ACA AAC GTA TCT GCT CCA GAT CAG CTG AGC TTG Ala Leu Leu Lys Gly Thr Asn Val Ser Ala Pro Asp Gln Leu Ser Leu 295 300 305	1266
GCA CTG GCT TGG AAC CGC GTG GAC ATA GCA CGA AGC CAG ATC TTT GTC Ala Leu Ala Trp Asn Arg Val Asp Ile Ala Arg Ser Gln Ile Phe Val 310 315 320	1314
TTT GGG CCC CAC TGG ACG CCC CTG GGA AGC CTG GCA CCC CCG ACG GAC Phe Gly Pro His Trp Thr Pro Leu Gly Ser Leu Ala Pro Pro Thr Asp 325 330 335	1362

AGC AAA GCC ACG GAG AAG GAG AAG AAG CCA CCC ATG GCC ACC ACC AAG Ser Lys Ala Thr Glu Lys Glu Lys Lys Pro Pro Met Ala Thr Thr Lys 340 345 350 355	1410
GGA GGA AGA GGA AAA GGG AAA GGC AAG AAG AAA GGG AAA GTG AAA GAG Gly Gly Arg Gly Lys Gly Lys Gly Lys Lys Gly Lys Val Lys Glu 360 365 370	1458
GAA GTG GAG GAA GAA ACT GAC CCC CGG AAG ATA GAG CTG CTG AAC TGG Glu Val Glu Glu Glu Thr Asp Pro Arg Lys Ile Glu Leu Leu Asn Trp 375 380 385	1506
GTG AAT GCT TTG GAG CAA GCG ATG CTA GAT GCT TTA GTC TTA GAT CGT Val Asn Ala Leu Glu Gln Ala Met Leu Asp Ala Leu Val Leu Asp Arg 390 395 400	1554
GTC GAC TTT GTG AAG CTC CTG ATT GAA AAC GGA GTG AAC ATG CAA CAC Val Asp Phe Val Lys Leu Ile Glu Asn Gly Val Asn Met Gln His 405 410 415	1602
TTT CTG ACC ATT CCG AGG CTG GAG GAG CTT TAT AAC ACA AGA CTG GGT Phe Leu Thr Ile Pro Arg Leu Glu Glu Leu Tyr Asn Thr Arg Leu Gly 420 425 430 435	1650
CCA CCA AAC ACA CTT CAT CTG CTG GTG AGG GAT GTG AAA AAG AGC AAC Pro Pro Asn Thr Leu His Leu Leu Val Arg Asp Val Lys Lys Ser Asn 440 445 450	1698
CTT CCG CCT GAT TAC CAC ATC AGC CTC ATA GAC ATC GGG CTC GTG CTG Leu Pro Pro Asp Tyr His Ile Ser Leu Ile Asp Ile Gly Leu Val Leu 455 460 465	1746
GAG TAC CTC ATG GGA GGA GCC TAC CGC TGC AAC TAC ACT CGG AAA AAC Glu Tyr Leu Met Gly Gly Ala Tyr Arg Cys Asn Tyr Thr Arg Lys Asn 470 475 480	1794
TTT CGG ACC CTT TAC AAC AAC TTG TTT GGA CCA AAG AGG CCT AAA GCT Phe Arg Thr Leu Tyr Asn Asn Leu Phe Gly Pro Lys Arg Pro Lys Ala 485 490 495	1842
CTT AAA CTT CTG GGA ATG GAA GAT GAT GAG CCT CCA GCT AAA GGG AAG Leu Lys Leu Leu Gly Met Glu Asp Asp Glu Pro Pro Ala Lys Gly Lys 500 505 510 515	1890
AAA AAA AAA AAA AAG AAA AAG GAG GAA GAG ATC GAC ATT GAT GTG GAC Lys Lys Lys Lys Lys Lys Lys Glu Glu Glu Ile Asp Ile Asp Val Asp 520 525 530	1938
GAC CCT GCC GTG AGT CGG TTC CAG TAT CCC TTC CAC GAG CTG ATG GTG Asp Pro Ala Val Ser Arg Phe Gln Tyr Pro Phe His Glu Leu Met Val 535 540 545	1986
TGG GCA GTG CTG ATG AAA CGC CAG AAA ATG GCA GTG TTC CTC TGG CAG Trp Ala Val Leu Met Lys Arg Gln Lys Met Ala Val Phe Leu Trp Gln 550 555 560	2034
CGA GGG GAA GAG AGC ATG GCC AAG GCC CTG GTG GCC TGC AAG CTC TAC Arg Gly Glu Glu Ser Met Ala Lys Ala Leu Val Ala Cys Lys Leu Tyr 565 570 575	2082
AAG GCC ATG GCC CAC GAG TCC TCC GAG AGT GAT CTG GTG GAT GAC ATC Lys Ala M t Ala His Glu Ser Ser Glu Ser Asp Leu Val Asp Asp Ile 580 585 590 595	2130

TCC CAG GAC TTG GAT AAC AAT TCC AAA GAC TTC GGC CAG CTT GCT TTG Ser Gln Asp Leu Asp Asn Asn Ser Lys Asp Ph Gly Gln Leu Ala Leu 600 605 610	2178
GAG TTA TTA GAC CAG TCC TAT AAG CAT GAC GAG CAG ATC GCT ATG AAA Glu Leu Leu Asp Gln S r Tyr Lys His Asp Glu Gln Il Ala Met Lys 615 620 625	2226
CTC CTG ACC TAC GAG CTG AAA AAC TGG AGC AAC TCG ACC TGC CTC AAA Leu Leu Thr Tyr Glu Leu Lys Asn Trp Ser Asn Ser Thr Cys Leu Lys 630 635 640	2274
CTG GCC GTG GCA GCC AAA CAC CGG GAC TTC ATT GCT CAC ACC TGC AGC Leu Ala Val Ala Ala Lys His Arg Asp Phe Ile Ala His Thr Cys Ser 645 650 655	2322
CAG ATG CTG CTG ACC GAT ATG TGG ATG GGA AGA CTG CGG ATG CGG AAG Gln Met Leu Leu Thr Asp Met Trp Met Gly Arg Leu Arg Met Arg Lys 660 665 670 675	2370
AAC CCC GGC CTG AAG GTT ATC ATG GGG ATT CTT CTA CCC CCC ACC ATC Asn Pro Gly Leu Lys Val Ile Met Gly Ile Leu Leu Pro Pro Thr Ile 680 685 690	2418
TTG TTT TTG GAA TTT CGC ACA TAT GAT GAT TTC TCG TAT CAA ACA TCC Leu Phe Leu Glu Phe Arg Thr Tyr Asp Asp Phe Ser Tyr Gln Thr Ser 695 700 705	2466
AAG GAA AAC GAG GAT GGC AAA GAA AAA GAA GAG GAA AAT ACG GAT GCA Lys Glu Asn Glu Asp Gly Lys Glu Lys Glu Glu Glu Asn Thr Asp Ala 710 715 720	2514
AAT GCA GAT GCT GGC TCA AGA AAG GGG GAT GAG GAG AAC GAG CAT AAA Asn Ala Asp Ala Gly Ser Arg Lys Gly Asp Glu Glu Asn Glu His Lys 725 730 735	2562
AAA CAG AGA AGT ATT CCC ATC GGA ACA AAG ATC TGT GAA TTC TAT AAC Lys Gln Arg Ser Ile Pro Ile Gly Thr Lys Ile Cys Glu Phe Tyr Asn 740 745 750 755	2610
GCG CCC ATT GTC AAG TTC TGG TTT TAC ACA ATA TCA TAC TTG GGC TAC Ala Pro Ile Val Lys Phe Trp Phe Tyr Thr Ile Ser Tyr Leu Gly Tyr 760 765 770	2658
CTG CTG CTG TTT AAC TAC GTC ATC CTG GTG CGG ATG GAT GGC TGG CCG Leu Leu Leu Phe Asn Tyr Val Ile Leu Val Arg Met Asp Gly Trp Pro 775 780 785	2706
TCC CTC CAG GAG TGG ATC GTC ATC TCC TAC ATC GTG AGC CTG GCG TTA Ser Leu Gln Glu Trp Ile Val Ile Ser Tyr Ile Val Ser Leu Ala Leu 790 795 800	2754
GAG AAG ATA CGA GAG ATC CTC ATG TCA GAA CCA GGC AAA CTC AGC CAG Glu Lys Ile Arg Glu Ile Leu Met Ser Glu Pro Gly Lys Leu Ser Gln 805 810 815	2802
AAA ATC AAA GTT TGG CTT CAG GAG TAC TGG AAC ATC ACA GAT CTC GTG Lys Ile Lys Val Trp Leu Gln Glu Tyr Trp Asn Ile Thr Asp Leu Val 820 825 830 835	2850
GCC ATT TCC ACA TTC ATG ATT GGA GCA ATT CTT CGC CTA CAG AAC CAG Ala Ile Ser Thr Ph Met Ile Gly Ala Ile Leu Arg Leu Gln Asn Gln 840 845 850	2898

CCC Pro	TAC Tyr	ATG M t	GGC Gly 855	TAT Tyr	GGC Gly	CGG Arg	GTG Val	ATC Ile 860	TAC Tyr	TGT Cys	GTG Val	GAT Asp	ATC Ile 865	ATC Ile	TTC Phe	2946
TGG Trp	TAC Tyr	ATC Ile 870	CGT Arg	GTC Val	CTG Leu	GAC Asp	ATC Ile 875	TTT Phe	GGT Gly	GTC Val	AAC Asn	AAG Lys 880	TAT Tyr	CTG Leu	GGG Gly	2994
CCA Pro	TAC Tyr 885	GTG Val	ATG Met	ATG Met	ATT Ile	GGA Gly 890	AAG Lys	ATG Met	ATG Met	ATC Ile	GAC Asp 895	ATG Met	CTG Leu	TAC Tyr	TTT Phe	3042
GTG Val 900	GTC Val	ATC Ile	ATG Met	CTG Leu	GTC Val 905	GTG Val	CTC Leu	ATG Met	AGT Ser	TTC Phe 910	GGA Gly	GTA Val	GCC Ala	CGT Arg	CAA Gln 915	3090
GCC Ala	ATT Ile	CTG Leu	CAT His	CCA Pro 920	GAG Glu	GAG Glu	AAG Lys	CCC Pro	TCT Ser 925	TGG Trp	AAA Lys	CTG Leu	GCC Ala	CGA Arg 930	AAC Asn	3138
ATC Ile	TTC Phe	TAC Tyr	ATG Met 935	CCC Pro	TAC Tyr	TGG Trp	ATG Met	ATC Ile 940	TAT Tyr	GGA Gly	GAG Glu	GTG Val	TTT Phe 945	GCA Ala	GAC Asp	3186
CAG Gln	ATA Ile	GAC Asp 950	CTC Leu	TAC Tyr	GCC Ala	ATG Met	GAA Glu 955	ATT Ile	AAT Asn	CCT Pro	CCT Pro	TGT Cys 960	GGT Gly	GAG Glu	AAC Asn	3234
CTA Leu	TAT Tyr 965	GAT Asp	GAG Glu	GAG Glu	GGC Gly	AAG Lys 970	CGG Arg	CTT Leu	CCT Pro	CCC Pro	TGT Cys 975	ATC Ile	CCC Pro	GGC Gly	GCC Ala	3282
TGG Trp 980	CTC Leu	ACT Thr	CCA Pro	GCA Ala	CTC Leu 985	ATG Met	GCG Ala	TGC Cys	TAT Tyr	CTA Leu 990	CTG Leu	GTC Val	GCC Ala	AAC Asn	ATC Ile 995	3330
CTG Leu	CTG Leu	GTG Val	AAC Asn 1000	CTG Leu	CTG Leu	ATT Ile	GCT Ala	GTG Val	TTC Phe 1005	AAC Asn	AAT Asn	ACT Thr	TTC Phe	TTT Phe 1010	GAA Glu	3378
GTA Val	AAA Lys	TCA Ser	ATA Ile 1015	TCC Ser	AAC Asn	CAG Gln	GTG Val	TGG Trp 1020	AAG Lys	TTC Phe	CAG Gln	CGA Arg	TAT Tyr 1025	CAG Gln	CTG Leu	3426
ATT Ile	ATG Met	ACA Thr 1030	TTT Phe	CAT His	GAC Asp	AGG Arg	CCA Pro 1035	GTC Val	CTG Leu	CCC Pro	CCA Pro	CCG Pro 1040	ATG Met	ATC Ile	ATT Ile	3474
TTA Leu	AGC Ser 1045	CAC His	ATC Ile	TAC Tyr	ATC Ile	ATC Ile 1050	ATT Ile	ATG Met	CGT Arg	CTC Leu	AGC Ser 1055	GGC Gly	CGC Arg	TGC Cys	AGG Arg	3522
AAA Lys 1060	AAG Lys	AGA Arg	GAA Glu	GGG Gly	GAC Asp 1065	CAA Gln	GAG Glu	GAA Glu	CGG Arg	GAT Asp 1070	CGT Arg	GGA Gly	TTG Leu	AAG Lys	CTC Leu 1075	3570
TTC Phe	CTT Leu	AGC Ser	GAC Asp	GAG Glu 1080	GAG Glu	CTA Leu	AAG Lys	AGG Arg	CTG Leu 1085	CAT His	GAG Glu	TTC Phe	GAG Glu 1090	GAG Glu	CAG Gln	3618
TGC Cys	GTG Val	CAG Gln	GAG Glu 1095	CAC His	TTC Phe	CGG Arg	GAG Glu	AAG Lys 1100	GAG Glu	GAT Asp	GAG Glu	CAG Gln	CAG Gln	TCG Ser	TCC Ser	3666

AGC GAC GAG CGC ATC CGG GTC ACT TCT GAA AGA GTT GAA AAT ATG TCA Ser Asp lu Arg Il Arg Val Thr S r Glu Arg Val Glu Asn Met Ser 1110 1115 1120	3714
ATG AGG TTG GAA GAA ATC AAT GAA AGA GAA ACT TTT ATG AAA ACT TCC Met Arg Leu Glu Glu Il Asn Glu Arg Glu Thr Phe Met Lys Thr Ser 1125 1130 1135	3762
CTG CAG ACT GTT GAC CTT CGA CTT GCT CAG CTA GAA GAA TTA TCT AAC Leu Gln Thr Val Asp Leu Arg Leu Ala Gln Leu Glu Glu Leu Ser Asn 1140 1145 1150 1155	3810
AGA ATG GTG AAT GCT CTT GAA AAT CTT GCG GGA ATC GAC AGG TCT GAC Arg Met Val Asn Ala Leu Glu Asn Leu Ala Gly Ile Asp Arg Ser Asp 1160 1165 1170	3858
CTG ATC CAG GCA CGG TCC CGG GCT TCT TCT GAA TGT GAG GCA ACG TAT Leu Ile Gln Ala Arg Ser Arg Ala Ser Ser Glu Cys Glu Ala Thr Tyr 1175 1180 1185	3906
CTT CTC CGG CAA AGC AGC ATC AAT AGC GCT GAT GGC TAC AGC TTG TAT Leu Leu Arg Gln Ser Ser Ile Asn Ser Ala Asp Gly Tyr Ser Leu Tyr 1190 1195 1200	3954
CGA TAT CAT TTT AAC GGA GAA GAG TTA TTA TTT GAG GAT ACA TCT CTC Arg Tyr His Phe Asn Gly Glu Glu Leu Leu Phe Glu Asp Thr Ser Leu 1205 1210 1215	4002
TCC ACG TCA CCA GGG ACA GGA GTC AGG AAA AAA ACC TGT TCC TTC CGT Ser Thr Ser Pro Gly Thr Gly Val Arg Lys Lys Thr Cys Ser Phe Arg 1220 1225 1230 1235	4050
ATA AAG GAA GAG AAG GAC GTG AAA ACG CAC CTA GTC CCA GAA TGT CAG Ile Lys Glu Glu Lys Asp Val Lys Thr His Leu Val Pro Glu Cys Gln 1240 1245 1250	4098
AAC AGT CTT CAC CTT TCA CTG GGC ACA AGC ACA TCA GCA ACC CCA GAT Asn Ser Leu His Leu Ser Leu Gly Thr Ser Thr Ser Ala Thr Pro Asp 1255 1260 1265	4146
GGC AGT CAC CTT GCA GTA GAT GAC TTA AAG AAC GCT GAA GAG TCA AAA Gly Ser His Leu Ala Val Asp Asp Leu Lys Asn Ala Glu Glu Ser Lys 1270 1275 1280	4194
TTA GGT CCA GAT ATT GGG ATT TCA AAG GAA GAT GAT GAA AGA CAG ACA Leu Gly Pro Asp Ile Gly Ile Ser Lys Glu Asp Asp Glu Arg Gln Thr 1285 1290 1295	4242
GAC TCT AAA AAA GAA GAA ACT ATT TCC CCA AGT TTA AAT AAA ACA GAT Asp Ser Lys Lys Glu Glu Thr Ile Ser Pro Ser Leu Asn Lys Thr Asp 1300 1305 1310 1315	4290
GTG ATA CAT GGA CAG GAC AAA TCA GAT GTT CAA AAC ACT CAG CTA ACA Val Ile His Gly Gln Asp Lys Ser Asp Val Gln Asn Thr Gln Leu Thr 1320 1325 1330	4338
GTG GAA ACG ACA AAT ATA GAA GGC ACT ATT TCC TAT CCC CTG GAA GAA Val Glu Thr Thr Asn Ile Glu Gly Thr Ile Ser Tyr Pro Leu Glu Glu 1335 1340 1345	4386
ACC AAA ATT ACA CGC TAT TTC CCC GAT GAA ACG ATC AAT GCT TGT AAA Thr Lys Ile Thr Arg Tyr Ph Pro Asp Glu Thr Ile Asn Ala Cys Lys 1350 1355 1360	4434

ACA ATG AAG TCC AGA AGC TTC GTC TAT TCC CGG GGA AGA AAG CTG GTC Thr Met Lys S r Arg Ser Phe Val Tyr Ser Arg Gly Arg Lys Leu Val 1365 1370 1375	4482
GGT GGG GTT AAC CAG GAT GTA GAG TAC AGT TCA ATC ACG GAC CAG CAA Gly Gly Val Asn Gln Asp Val Glu Tyr Ser Ser Ile Thr Asp Gln Gln 1380 1385 1390 1395	4530
TTG ACG ACG GAA TGG CAA TGC CAA GTT CAA AAG ATC ACG CGC TCT CAT Leu Thr Thr Glu Trp Gln Cys Gln Val Gln Lys Ile Thr Arg Ser His 1400 1405 1410	4578
AGC ACA GAT ATT CCT TAC ATT GTG TCG GAA GCT GCA GTG CAA GCT GAG Ser Thr Asp Ile Pro Tyr Ile Val Ser Glu Ala Ala Val Gln Ala Glu 1415 1420 1425	4626
CAA AAA GAG CAG TTT GCA GAT ATG CAA GAT GAA CAC CAT GTC GCT GAA Gln Lys Glu Gln Phe Ala Asp Met Gln Asp Glu His His Val Ala Glu 1430 1435 1440	4674
GCA ATT CCT CGA ATC CCT CGC TTG TCC CTA ACC ATT ACT GAC AGA AAT Ala Ile Pro Arg Ile Pro Arg Leu Ser Leu Thr Ile Thr Asp Arg Asn 1445 1450 1455	4722
GGG ATG GAA AAC TTA CTG TCT GTG AAG CCA GAT CAA ACT TTG GGA TTC Gly Met Glu Asn Leu Leu Ser Val Lys Pro Asp Gln Thr Leu Gly Phe 1460 1465 1470 1475	4770
CCA TCT CTC AGG TCA AAA AGT TTA CAT GGA CAT CCT AGG AAT GTG AAA Pro Ser Leu Arg Ser Lys Ser Leu His Gly His Pro Arg Asn Val Lys 1480 1485 1490	4818
TCC ATT CAG GGA AAG TTA GAC AGA TCT GGA CAT GCC AGT AGT GTA AGC Ser Ile Gln Gly Lys Leu Asp Arg Ser Gly His Ala Ser Ser Val Ser 1495 1500 1505	4866
AGC TTA GTA ATT GTG TCT GGA ATG ACA GCA GAA GAA AAA AAG GTT AAG Ser Leu Val Ile Val Ser Gly Met Thr Ala Glu Glu Lys Lys Val Lys 1510 1515 1520	4914
AAA GAG AAA GCT TCC ACA GAA ACT GAA TGC T AGTCTGTTTT GTTTCTTTAA Lys Glu Lys Ala Ser Thr Glu Thr Glu Cys 1525 1530	4965
TTTTTTTTTTT TAACAGTCAG AAACCCACTA ATGGGTGTCA TCTTGGCCCA TCCTAAACAC	5025
ATMTCCAATT TCCTAAAAAC ATTTTCCCTT	5055

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1533 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Tyr	Ile	Arg	Val	Ser	Tyr	Asp	Thr	Lys	Pro	Asp	Ser	Leu	Leu	His
1				5					10					15	
Leu	Met	Val	Lys	Asp	Trp	Gln	Leu	Glu	Leu	Pro	Lys	Leu	Leu	Ile	Ser
	20						25						30		



Val His Gly Gly Leu Gln Asn Phe Glu M t Gln Pro Lys Leu Lys Gln  
 35 40 45  
 Val Phe Gly Lys Gly Leu Ile Lys Ala Ala Met Thr Thr Gly Ala Trp  
 50 55 60  
 Ile Ph Thr Gly Gly Val Ser Thr Gly Val Ile Ser His Val Gly Asp  
 65 70 75 80  
 Ala Leu Lys Asp His Ser Ser Lys Ser Arg Gly Arg Val Cys Ala Ile  
 85 90 95  
 Gly Ile Ala Pro Trp Gly Ile Val Glu Asn Lys Glu Asp Leu Val Gly  
 100 105 110  
 Lys Asp Val Thr Arg Val Tyr Gln Thr Met Ser Asn Pro Leu Ser Lys  
 115 120 125  
 Leu Ser Val Leu Asn Asn Ser His Thr His Phe Ile Leu Ala Asp Asn  
 130 135 140  
 Gly Thr Leu Gly Lys Tyr Gly Ala Glu Val Lys Leu Arg Arg Leu Leu  
 145 150 155 160  
 Glu Lys His Ile Ser Leu Gln Lys Ile Asn Thr Arg Leu Gly Gln Gly  
 165 170 175  
 Val Pro Leu Val Gly Leu Val Val Glu Gly Gly Pro Asn Val Val Ser  
 180 185 190  
 Ile Val Leu Glu Tyr Leu Gln Glu Glu Pro Pro Ile Pro Val Val Ile  
 195 200 205  
 Cys Asp Gly Ser Gly Arg Ala Ser Asp Ile Leu Ser Phe Ala His Lys  
 210 215 220  
 Tyr Cys Glu Glu Gly Gly Ile Ile Asn Glu Ser Leu Arg Glu Gln Leu  
 225 230 235 240  
 Leu Val Thr Ile Gln Lys Thr Phe Asn Tyr Asn Lys Ala Gln Ser His  
 245 250 255  
 Gln Leu Phe Ala Ile Ile Met Glu Cys Met Lys Lys Lys Glu Leu Val  
 260 265 270  
 Thr Val Phe Arg Met Gly Ser Glu Gly Gln Gln Asp Ile Glu Met Ala  
 275 280 285  
 Ile Leu Thr Ala Leu Leu Lys Gly Thr Asn Val Ser Ala Pro Asp Gln  
 290 295 300  
 Leu Ser Leu Ala Leu Ala Trp Asn Arg Val Asp Ile Ala Arg Ser Gln  
 305 310 315 320  
 Ile Phe Val Phe Gly Pro His Trp Thr Pro Leu Gly Ser Leu Ala Pro  
 325 330 335  
 Pro Thr Asp Ser Lys Ala Thr Glu Lys Glu Lys Lys Pro Pro Met Ala  
 340 345 350  
 Thr Thr Lys Gly Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys Gly Lys  
 355 360 365

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Val 370	Lys	Glu	Glu	Val	Glu 375	Glu	Thr	Asp	Pro	Arg 380	Lys	Ile	Glu	Leu
Leu 385	Asn	Trp	Val	Asn	Ala 390	Leu	Glu	Gln	Ala	M t 395	L u	Asp	Ala	Leu Val 400
L u	Asp	Arg	Val	Asp 405	Phe	Val	Lys	Leu	Leu 410	Ile	Glu	Asn	Gly	Val Asn 415
Met	Gln	His	Phe 420	Leu	Thr	Ile	Pro	Arg 425	Leu	Glu	Glu	Leu	Tyr 430	Asn Thr
Arg	Leu	Gly 435	Pro	Pro	Asn	Thr	Leu 440	His	Leu	Leu	Val	Arg 445	Asp	Val Lys
Lys	Ser 450	Asn	Leu	Pro	Pro	Asp 455	Tyr	His	Ile	Ser	Leu 460	Ile	Asp	Ile Gly
Leu 465	Val	Leu	Glu	Tyr	Leu 470	Met	Gly	Gly	Ala	Tyr 475	Arg	Cys	Asn	Tyr Thr 480
Arg	Lys	Asn	Phe	Arg 485	Thr	Leu	Tyr	Asn	Asn 490	Leu	Phe	Gly	Pro	Lys Arg 495
Pro	Lys	Ala	Leu 500	Lys	Leu	Leu	Gly	Met 505	Glu	Asp	Asp	Glu	Pro 510	Pro Ala
Lys	Gly	Lys 515	Lys	Lys	Lys	Lys	Lys 520	Lys	Lys	Glu	Glu	Glu 525	Ile	Asp Ile
Asp	Val 530	Asp	Asp	Pro	Ala	Val 535	Ser	Arg	Phe	Gln	Tyr 540	Pro	Phe	His Glu
Leu 545	Met	Val	Trp	Ala	Val 550	Leu	Met	Lys	Arg	Gln 555	Lys	Met	Ala	Val Phe 560
Leu	Trp	Gln	Arg	Gly 565	Glu	Glu	Ser	Met	Ala 570	Lys	Ala	Leu	Val	Ala Cys 575
Lys	Leu	Tyr	Lys 580	Ala	Met	Ala	His	Glu 585	Ser	Ser	Glu	Ser	Asp 590	Leu Val
Asp	Asp	Ile 595	Ser	Gln	Asp	Leu	Asp 600	Asn	Asn	Ser	Lys	Asp 605	Phe	Gly Gln
Leu	Ala	Leu	Glu	Leu	Leu	Asp 615	Gln	Ser	Tyr	Lys	His 620	Asp	Glu	Gln Ile
Ala 625	Met	Lys	Leu	Leu	Thr 630	Tyr	Glu	Leu	Lys	Asn 635	Trp	Ser	Asn	Ser Thr 640
Cys	Leu	Lys	Leu	Ala 645	Val	Ala	Ala	Lys	His 650	Arg	Asp	Phe	Ile	Ala His 655
Thr	Cys	Ser	Gln 660	Met	Leu	Leu	Thr	Asp 665	Met	Trp	Met	Gly	Arg 670	Leu Arg
Met	Arg	Lys 675	Asn	Pro	Gly	Leu	Lys 680	Val	Ile	Met	Gly	Ile 685	Leu	Leu Pro
Pro	Thr 690	Il	Leu	Ph	Leu	Glu 695	Ph	Arg	Thr	Tyr	Asp 700	Asp	Ph	Ser Tyr

[illegible]

Gln Thr Ser Lys Glu Asn Glu Asp Gly Lys Glu Lys Glu Glu Glu Asn  
 705 710 715 720  
 Thr Asp Ala Asn Ala Asp Ala Gly Ser Arg Lys Gly Asp Glu Glu Asn  
 725 730 735  
 Glu His Lys Lys Gln Arg Ser Ile Pro Ile Gly Thr Lys Ile Cys Glu  
 740 745 750  
 Phe Tyr Asn Ala Pro Ile Val Lys Phe Trp Phe Tyr Thr Ile Ser Tyr  
 755 760 765  
 Leu Gly Tyr Leu Leu Leu Phe Asn Tyr Val Ile Leu Val Arg Met Asp  
 770 775 780  
 Gly Trp Pro Ser Leu Gln Glu Trp Ile Val Ile Ser Tyr Ile Val Ser  
 785 790 795 800  
 Leu Ala Leu Glu Lys Ile Arg Glu Ile Leu Met Ser Glu Pro Gly Lys  
 805 810 815  
 Leu Ser Gln Lys Ile Lys Val Trp Leu Gln Glu Tyr Trp Asn Ile Thr  
 820 825 830  
 Asp Leu Val Ala Ile Ser Thr Phe Met Ile Gly Ala Ile Leu Arg Leu  
 835 840 845  
 Gln Asn Gln Pro Tyr Met Gly Tyr Gly Arg Val Ile Tyr Cys Val Asp  
 850 855 860  
 Ile Ile Phe Trp Tyr Ile Arg Val Leu Asp Ile Phe Gly Val Asn Lys  
 865 870 875 880  
 Tyr Leu Gly Pro Tyr Val Met Met Ile Gly Lys Met Met Ile Asp Met  
 885 890 895  
 Leu Tyr Phe Val Val Ile Met Leu Val Val Leu Met Ser Phe Gly Val  
 900 905 910  
 Ala Arg Gln Ala Ile Leu His Pro Glu Glu Lys Pro Ser Trp Lys Leu  
 915 920 925  
 Ala Arg Asn Ile Phe Tyr Met Pro Tyr Trp Met Ile Tyr Gly Glu Val  
 930 935 940  
 Phe Ala Asp Gln Ile Asp Leu Tyr Ala Met Glu Ile Asn Pro Pro Cys  
 945 950 955 960  
 Gly Glu Asn Leu Tyr Asp Glu Glu Gly Lys Arg Leu Pro Pro Cys Ile  
 965 970 975  
 Pro Gly Ala Trp Leu Thr Pro Ala Leu Met Ala Cys Tyr Leu Leu Val  
 980 985 990  
 Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Val Phe Asn Asn Thr  
 995 1000 1005  
 Phe Phe Glu Val Lys Ser Ile Ser Asn Gln Val Trp Lys Phe Gln Arg  
 1010 1015 1020  
 Tyr Gln Leu Ile Met Thr Phe His Asp Arg Pro Val Leu Pro Pro Pro  
 1025 1030 1035 1040

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Lys Leu Val Gly Gly Val Asn Gln Asp Val Glu Tyr Ser Ser Ile Thr  
1380 1385 1390

[illegible]